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O75635

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Entry information

Entry name **SPB7_HUMAN**
 Primary accession number **O75635**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 41, February 2003
 Sequence was last modified in Release 41, February 2003
 Annotations were last modified in Release 41, February 2003

Name and origin of the protein

Protein name **Megsin**
 Synonyms **TP55** —
Serpin B7
 Gene name **SERPINB7**
 From Homo sapiens (Human) [TaxID: 9606]
 Taxonomy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

References

[1] SEQUENCE FROM NUCLEIC ACID.

MEDLINE=97326116; PubMed=9182567; [NCBI, ExPASy, EBI, Israel, Japan]
Tsujimoto M., Tsuruoka N., Ishida N., Kurihara T., Iwasa F., Yamashiro K., Rogi T., Kodama S.,
Katsuragi N., Adachi M., Katayama T., Nakao M., Yamaichi K., Hashino J., Haruyama M., Miura K.,
Nakanishi T., Nakazato H., Teramura M., Mizoguchi H., Yamaguchi N.;
 "Purification, cDNA cloning, and characterization of a new serpin with megakaryocyte maturation activity."
J. Biol. Chem. 272:15373-15380(1997).

[2] SEQUENCE FROM NUCLEIC ACID.

TISSUE=Mesangial cells;
 MEDLINE=98376492; PubMed=9710452; [NCBI, ExPASy, EBI, Israel, Japan]
Miyata T., Nangaku M., Suzuki D., Inagi R., Uragami K., Sakai H., Okubo K., Kurokawa K.;
 "A mesangium-predominant gene, megsin, is a new serpin upregulated in IgA nephropathy."
J. Clin. Invest. 102:828-836(1998).

Comments

- **FUNCTION:** Might function as an inhibitor of Lys-specific proteases. Might influence the maturation of megakaryocytes via its action as a serpin.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **TISSUE SPECIFICITY:** Predominantly expressed in mesangial cells.
- **SIMILARITY:** Belongs to the serpin family. Ov-serpin subfamily.

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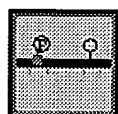
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Cross-references

| | |
|--------------|--|
| EMBL | D88575; BAA31232.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AF027866; AAC64506.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| HSSP | P05619; 1HLE. [HSSP ENTRY / PDB] |
| Genew | HGNC:13902 ; SERPINB7. |
| CleanEx | HGNC:13902 ; SERPINB7. |
| GeneCards | SERPINB7 . |
| GeneLynx | SERPINB7 ; Homo sapiens. |
| GenAtlas | SERPINB7 . |
| MIM | 603357 [NCBI / EBI]. |
| GO | GO:0004868 ; Molecular function: serpin (<i>traceable author statement</i>). |
| SOURCE | SERPINB7 ; Homo sapiens. |
| Ensembl | O75635; Homo sapiens. [Entry / Contig view] |
| InterPro | IPR000215 ; Serpin. Graphical view of domain structure . |
| Pfam | PF00079 ; serpin; 1. |
| SMART | SM00093 ; SERPIN; 1. |
| PROSITE | PS00284 ; SERPIN; 1. |
| ProDom | [Domain structure / List of seq. sharing at least 1 domain] |
| HOVERGEN | [Family / Alignment / Tree] |
| BLOCKS | O75635 . |
| ProtoNet | O75635 . |
| ProtoMap | O75635 . |
| PRESAGE | O75635 . |
| DIP | O75635 . |
| ModBase | O75635 . |
| SMR | O75635 ; 9A2CDB6C63CFF605. |
| SWISS-2DPAGE | Get region on 2D PAGE . |

Keywords

Serpin; **Serine protease inhibitor**.

Features

[Feature table viewer](#)

| Key | From | To | Length | Description |
|----------|------|-----|--------|---------------------------------|
| ACT_SITE | 347 | 348 | | REACTIVE BOND (BY SIMILARITY) . |

Sequence information

Length: **380** Molecular weight: **42904** CRC64: **9A2CDB6C63CFF605** [This is a checksum on the AA Da sequence]

| 10 | 20 | 30 | 40 | 50 | 60 |
|------------|------------|------------|------------|------------|------------|
| MASLAAANAE | FCFNLFREMD | DNQGNGNVFF | SSLSLFAALA | LVRLGAQDDS | LSQIDKLLHV |
| 70 | 80 | 90 | 100 | 110 | 120 |
| NTASGYGNSS | NSQSGLQSQL | KRVFSDINAS | HKDYDLSIVN | GLFAEKVYGF | HKDYIECAEK |
| 130 | 140 | 150 | 160 | 170 | 180 |
| LYDAKVERVD | FTNHLEDTRR | NINKWVENET | HGKIKNVIGE | GGISSAVMV | LVNAVYFKGK |
| 190 | 200 | 210 | 220 | 230 | 240 |
| WQSAFTKSET | INCHFKSPKC | SGKAVAMMHQ | ERKFNLVIE | DPSMKILELR | YNGGINMYVL |
| 250 | 260 | 270 | 280 | 290 | 300 |
| LPENDLSEIE | NKLTFQNLME | WTNPRRMTSK | YVEVFFPQFK | IEKNYEMKQY | LRALGLKDIF |
| 310 | 320 | 330 | 340 | 350 | 360 |
| DESKADLSGI | ASGGRLYISR | MMHKSYIEVT | EEGTEATAAT | GSNIVEKQLP | QSTLFRADHP |
| 370 | 380 | | | | |
| FLFVIRKDDI | ILFSGKVSCP | | | | |

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[ScanProsite](#), [MotifScan](#)



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